CLAIMS

What is Claimed is:

1. A method for obtaining a prognosis for a subject having, or at risk of developing, an inflammatory condition, the method comprising determining a genotype of said subject which includes one or more polymorphic sites in the subject's protein C sequence; EPCR sequence or a combination thereof, wherein said genotype is indicative of an ability of the subject to recover from the inflammatory condition.

2. The method of claim 1, wherein the polymorphic site is at position 4732 of SEQ ID NO:1; or position 4054 of SEQ ID NO:2; or a polymorphic site in linkage disequilibrium thereto.

3. The method of claim 1, wherein the polymorphic sites from both the Protein C sequence and EPCR sequence are combined, wherein said polymorphic sites are at two or more of position 4732 of SEQ ID NO:1; or position 4054 of SEQ ID NO:2; or position 2418 of SEQ ID NO:1; or a polymorphic site in linkage disequilibrium thereto.

4. The method of claim 2 or 3, wherein the polymorphic site in linkage disequilibrium with position 4732 is at position 4813, 6379, 6762, 7779, 8058, 8915 or 12228 of SEQ ID NO: 1.

5. The method of claim 2 or 3, wherein the polymorphic site in linkage disequilibrium with position 4054 is at position 2973, 3063, 3402, 4946, 5515 or 6196 of SEQ ID NO: 2.

6. The method of claim 3, wherein the polymorphic site in linkage disequilibrium with position 2418 is at position 1386, 2583 or 3920 in SEQ ID NO: 1.

7. The method of claim 2 or 3, wherein the polymorphic site in linkage disequilibrium with position 4732 includes a combination of two polymorphic sites, which sites occur at any of the following combinations of positions in SEQ ID NO:1:

9198 and 5867;
9198 and 4800;
3220 and 5867; and
3220 and 4800.

8. The method of claim 3, wherein the polymorphic site in linkage disequilibrium with position 2418 includes a combination of two polymorphic sites, which sites

occur at any of the following combinations of positions in SEQ ID NO:1:

5867 and 2405;
5867 and 4919;
5867 and 4956;
5867 and 6187;
5867 and 12109;
4800 and 2405;
4800 and 4919;
4800 and 4956;
4800 and 6187; and
4800 and 12109.

9. The method of any one of claims 1-8, further comprising comparing the genotype so determined with known genotypes which are known to be indicative of a prognosis for recovery from:

(i) the subject's type of inflammatory condition; or

(ii) another inflammatory condition.

10. The method of any one of claims 1-9, further comprising obtaining protein C sequence information or EPCR sequence information for the subject.

11. The method of any one of claims 1-9, wherein the genotype is determined using a nucleic acid sample from the subject.

12. The method of claim 11, further comprising obtaining the nucleic acid sample from the subject.

13. The method of any one of claims 1-12, wherein said genotype is determined using one or more of the following techniques:

(a) restriction fragment length analysis;

(b) sequencing;

(c) hybridization;

(d) oligonucleotide ligation assay;

(e) ligation rolling circle amplification;

(f) 5′ nuclease assay;

(g) polymerase proofreading methods;

(h) allele specific PCR; and

(i) reading sequence data.

14. The method of any one of claims 1-13, wherein the genotype of the subject is indicative of a decreased ability to recover from the inflammatory condition.

15. The method of claim 14, wherein the subject is critically ill and the genotype is

indicative of a prognosis of severe cardiovascular or respiratory dysfunction.

16. The method of claim 14 or 15, wherein the genotype comprises at least one of the following single polymorphic nucleotides or combinations of polymorphic nucleotides at the indicated positions of SEQ ID NO: 1:

4732 C;
4813 A;
6379 G;
6762 A;
7779 C;
8058 T;
8915 T;
12228 T;
9198 C and 5867 A;
9198 C and 4800 G;
3220 A and 5867 A; and
3220 A and 4800 G

or

1386 T;
2418 A;
2583 A;
3920 T;
5867 A and 2405 T;
5867 A and 4919 A;
5867 A and 4956 T;
5867 A and 6187 C;
5867 A and 12109 T;
4800 G and 2405 T;
4800 G and 4919 A;
4800 G and 4956 T;
4800 G and 6187 C; and
4800 G and 12109 T.

17. The method of claim 14 or 15, the genotype comprises at least one of the following EPCR polymorphic nucleotides at the indicated positions of SEQ ID NO: 2:

6196 G;
5515 T;
4946 T;
4054 T;
3402 G;
3063 G; and
2973 C.

18. The method of any one of claims 1-13, wherein the genotype of the subject is indicative of an increased ability to recover from the inflammatory condition.

19. The method of claim 18, wherein the subject is critically ill and the genotype is indicative of a prognosis of mild cardiovascular or respiratory dysfunction.

20. The method of claim 18 or 19, wherein the genotype comprises at least one of the following single polymorphic nucleotides or combinations of polymorphic nucleotides at the indicated positions of SEQ ID NO: 1:

4732 T;
4813 G;
6379 A;
6762 G;
7779 -;
8058 C;
8915 G;
12228 C;
9198 A and 5867 G;
9198 A and 4800 C;
3220 G and 5867 G; and
3220 G and 4800 C

or

1386 C;
2418 G;
2583 T;
3920 C;
5867 G and 2405 C;
5867 G and 4919 G;
5867 G and 4956 C;
5867 G and 6187 T;
5867 G and 12109 C;
4800 C and 2405 C;
4800 C and 4919 G;
4800 C and 4956 C;
4800 C and 6187 T; and
4800 C and 12109 C.

21. The method of claim 18 or 19, the genotype comprises at least one of the following EPCR polymorphic nucleotides at the indicated positions of SEQ ID NO: 2:

6196 C;
5515 C;
4946 C;
4054 C;
3402 C;
3063 A; and
2973 T.

22. The method of any one of claims 1-21, wherein the inflammatory condition is

selected from the group consisting of: sepsis, septicemia, pneumonia, septic shock, systemic inflammatory response syndrome (SIRS), Acute Respiratory Distress Syndrome (ARDS), acute lung injury, aspiration pneumanitis, infection, pancreatitis, bacteremia, peritonitis, abdominal abscess, inflammation due to trauma, inflammation due to surgery, chronic inflammatory disease, ischemia, ischemia-reperfusion injury of an organ or tissue, tissue damage due to disease, tissue damage due to chemotherapy or radiotherapy, and reactions to ingested, inhaled, infused, injected, or delivered substances, glomerulonephritis, bowel infection, opportunistic infections, and for subjects undergoing major surgery or dialysis, subjects who are immunocompromised, subjects on immunosuppressive agents, subjects with HIV/AIDS, subjects with suspected endocarditis, subjects with fever, subjects with fever of unknown origin, subjects with cystic fibrosis, subjects with diabetes mellitus, subjects with chronic renal failure, subjects with bronchiectasis, subjects with chronic obstructive lung disease, chronic bronchitis, emphysema, or asthma, subjects with febrile neutropenia, subjects with meningitis, subjects with septic arthritis, subjects with urinary tract infection, subjects with necrotizing fasciitis, subjects with other suspected Group A streptococcus infection, subjects who have had a splenectomy, subjects with recurrent or suspected enterococcus infection, other medical and surgical conditions associated with increased risk of infection, Gram positive sepsis, Gram negative sepsis, culture negative sepsis, fungal sepsis, meningococcemia, post-pump syndrome, cardiac stun syndrome, myocardial infarction, stroke, congestive heart failure, hepatitis, epiglotittis, E. coli 0157:H7, malaria, gas gangrene, toxic shock syndrome, pre-eclampsia, eclampsia, HELP syndrome, mycobacterial tuberculosis, Pneumocystic carinii, pneumonia, Leishmaniasis, hemolytic uremic syndrome/thrombotic thrombocytopenic purpura, Dengue hemorrhagic fever, pelvic inflammatory disease, Legionella, Lyme disease, Influenza A, Epstein-Barr virus, encephalitis, inflammatory diseases and autoimmunity including Rheumatoid arthritis, osteoarthritis, progressive systemic sclerosis, systemic lupus erythematosus, inflammatory bowel disease, idiopathic pulmonary fibrosis, sarcoidosis, hypersensitivity pneumonitis, systemic vasculitis, Wegener's granulomatosis, transplants including heart, liver, lung kidney bone marrow, graft-versus-host disease, transplant rejection, sickle cell anemia, nephrotic syndrome,

toxicity of agents such as OKT3, cytokine therapy, and cirrhosis.

23. The method of any one of claims 1-22, wherein the inflammatory condition is SIRS.

24. A method of identifying a polymorphism in a protein C sequence that correlates with prognosis of recovery from an inflammatory condition, the method comprising:

a) obtaining protein C sequence or EPCR sequence information from a group of subjects having an inflammatory condition;

b) identifying at least one polymorphic nucleotide position in the protein C sequence or EPCR sequence in the subjects;

c) determining a genotypes at the polymorphic site for individual subjects in the group;

d) determining recovery capabilities of individual subjects in the group from the inflammatory condition; and

e) correlating the genotypes determined in step (c) with the recovery capabilities determined in step (d)

thereby identifying said protein C or EPCR polymorphisms that correlate with recovery.

25. The method of claim 24, wherein the inflammatory condition is selected from the group consisting of: sepsis, septicemia, pneumonia, septic shock, systemic inflammatory response syndrome (SIRS), Acute Respiratory Distress Syndrome (ARDS), acute lung injury, aspiration pneumanitis, infection, pancreatitis, bacteremia, peritonitis, abdominal abscess, inflammation due to trauma, inflammation due to surgery, chronic inflammatory disease, ischemia, ischemia-reperfusion injury of an organ or tissue, tissue damage due to disease, tissue damage due to chemotherapy or radiotherapy, and reactions to ingested, inhaled, infused, injected, or delivered substances, glomerulonephritis, bowel infection, opportunistic infections, and for subjects undergoing major surgery or dialysis, subjects who are immunocompromised, subjects on immunosuppressive agents, subjects with HIV/AIDS, subjects with suspected endocarditis, subjects with fever, subjects with fever of unknown origin, subjects with cystic fibrosis, subjects with diabetes mellitus, subjects with chronic renal failure, subjects with bronchiectasis, subjects with chronic obstructive lung disease, chronic bronchitis, emphysema, or

asthma, subjects with febrile neutropenia, subjects with meningitis, subjects with septic arthritis, subjects with urinary tract infection, subjects with necrotizing fasciitis, subjects with other suspected Group A streptococcus infection, subjects who have had a splenectomy, subjects with recurrent or suspected enterococcus infection, other medical and surgical conditions associated with increased risk of infection, Gram positive sepsis, Gram negative sepsis, culture negative sepsis, fungal sepsis, meningococcemia, post-pump syndrome, cardiac stun syndrome, myocardial infarction, stroke, congestive heart failure, hepatitis, epiglotittis, E. coli 0157:H7, malaria, gas gangrene, toxic shock syndrome, pre-eclampsia, eclampsia, HELP Syndrome, mycobacterialtuberculosis, Pneumocystic carinii, pneumonia, Leishmaniasis, hemolytic uremic syndrome/thrombotic thrombocytopenic purpura, Dengue hemorrhagic fever, pelvic inflammatory disease, Legionella, Lyme disease, Influenza A, Epstein-Barr virus, encephalitis, inflammatory diseases and autoimmunity including Rheumatoid arthritis, osteoarthritis, progressive systemic sclerosis, systemic lupus erythematosus, inflammatory bowel disease, idiopathic pulmonary fibrosis, sarcoidosis, hypersensitivity pneumonitis, systemic vasculitis, Wegener's granulomatosis, transplants including heart, liver, lung kidney bone marrow, graft-versus-host disease, transplant rejection, sickle cell anemia, nephrotic syndrome, toxicity of agents such as OKT3, cytokine therapy, and cirrhosis.

26. A kit for determining a genotype at a defined nucleotide position within a polymorphic site in a protein C sequence or an EPCR sequence in a subject to provide a prognosis of the subject's ability to recover from an inflammatory condition, the kit comprising:

(a) a restriction enzyme capable of distinguishing alternate nucleotides at the polymorphic site; or

(b) a labeled oligonucleotide having sufficient complementary to the polymorphic site so as to be capable of hybridizing distinctively to said alternate.

27. The kit of claim 26, wherein the polymorphic sites are at one or more of positions 4732 of SEQ ID NO:1, 4054 of SEQ ID NO:2, or a polymorphic site in linkage disequilibrium thereto.

28. The kit of claim 26, wherein the kit is suitable for determining genotype at one or

more nucleotide positions within each of the protein C sequence or the EPCR sequence, wherein said polymorphic sites are at one or more of positions 4732 of SEQ ID NO:1, 4054 of SEQ ID NO:2; 2418 of SEQ ID NO:1; or a polymorphic site in linkage disequilibrium thereto.

29. The kit of claim 26, 27 or 28 further comprising an oligonucleotide or a set of oligonucleotides operable to amplify a region including the polymorphic site.

30. The kit of claim 29, further comprising a polymerization agent.

31. The kit of any one of claims 26-30, further comprising instructions for using the kit to determine genotype.

32. A method for selecting a group of subjects for determining the efficacy of a candidate drug known or suspected of being useful for the treatment of an inflammatory condition, the method comprising determining a genotype at one or more polymorphic sites in the protein C sequence or EPCR sequence for each subject, wherein said genotype is indicative of the subject's ability to recover from the inflammatory condition and sorting subjects based on their genotype.

33. The method of claim 32 further comprising, administering the candidate drug to the subjects or a subset of subjects and determining each subject's ability to recover from the inflammatory condition.

34. The method of claim 33, further comprising comparing subject response to the candidate drug based on genotype of the subject.

35. A method of treating an inflammatory condition in a subject in need thereof, the method comprising administering to the subject an anti-inflammatory agent or an anti-coagulant agent, wherein said subject has a protein C sequence or EPCR sequence risk genotype.

36. A method of treating an inflammatory condition in a subject in need thereof, the method comprising:

(a) selecting a subject having a risk genotype in their protein C sequence or EPCR sequence; and

(b) administering to said subject an anti-inflammatory agent or an anti-coagulant agent.

37. A method of treating a subject with an inflammatory condition by administering an anti-inflammatory agent or an anti-coagulant agent, the method comprising administering the anti-inflammatory agent or the anti-coagulant agent to subjects

that have a risk genotype in their protein C sequence or EPCR sequence, wherein the risk genotype is predictive of increased responsiveness to the treatment of the inflammatory condition with the anti-inflammatory agent or the anti-coagulant agent.

38. A method of identifying a subject with increased responsiveness to treatment of an inflammatory condition with an anti-inflammatory agent or an anti-coagulant agent, comprising the step of screening a population of subjects to identify those subjects that have a risk genotype in their protein C sequence or EPCR sequence, wherein the identification of a subject with a risk genotype in their protein C sequence or EPCR sequence is predictive of increased responsiveness to the treatment of the inflammatory condition with the anti-inflammatory agent or the anti-coagulant agent.

39. A method of selecting a subject for the treatment of an inflammatory condition with an anti-inflammatory agent or an anti-coagulant agent, comprising the step of identifying a subject having a risk genotype in their protein C sequence or EPCR sequence, wherein the identification of a subject with the risk genotype is predictive of increased responsiveness to the treatment of the inflammatory condition with the anti-inflammatory agent or the anti-coagulant agent.

40. A method of treating an inflammatory condition in a subject, the method comprising administering an anti-inflammatory agent or an anti-coagulant agent to the subject, wherein said subject has a risk genotype in their protein C sequence or EPCR sequence.

41. A method of treating an inflammatory condition in a subject, the method comprising:

(a) identifying a subject having a risk genotype in their protein C sequence or EPCR sequence; and

(b) administering an anti-inflammatory agent or an anti-coagulant agent to the subject.

42. A use of an anti-inflammatory agent or an anti-coagulant in the manufacture of a medicament for the treatment of an inflammatory condition, wherein the subjects treated have a risk genotype in their protein C sequence or EPCR sequence.

43. A use of an anti-inflammatory agent or an anti-coagulant in the manufacture of a medicament for the treatment of an inflammatory condition in a subset of subjects,

wherein the subset of subjects have a risk genotype in their protein C sequence or EPCR sequence.

44. The method or use of any one of claims 35 to 43, further comprising determining the subject's APACHE II score as an assessment of subject risk.

45. The method or use of any one of claims 35 to 43, further comprising determining the number of organ system failures for the subject as an assessment of subject risk.

46. The method of claim 45, wherein the subject's APACHE II score is indicative of an increased risk when ≥ 25.

47. The method of claim 46, wherein 2 or more organ system failures are indicative of increased subject risk.

48. The method or use of any one of claims 35 to 47, wherein the inflammatory condition is selected from the group consisting of: sepsis, septicemia, pneumonia, septic shock, systemic inflammatory response syndrome (SIRS), Acute Respiratory Distress Syndrome (ARDS), acute lung injury, aspiration pneumanitis, infection, pancreatitis, bacteremia, peritonitis, abdominal abscess, inflammation due to trauma, inflammation due to surgery, chronic inflammatory disease, ischemia, ischemia-reperfusion injury of an organ or tissue, tissue damage due to disease, tissue damage due to chemotherapy or radiotherapy, and reactions to ingested, inhaled, infused, injected, or delivered substances, glomerulonephritis, bowel infection, opportunistic infections, and for subjects undergoing major surgery or dialysis, subjects who are immunocompromised, subjects on immunosuppressive agents, subjects with HIV/AIDS, subjects with suspected endocarditis, subjects with fever, subjects with fever of unknown origin, subjects with cystic fibrosis, subjects with diabetes mellitus, subjects with chronic renal failure, subjects with bronchiectasis, subjects with chronic obstructive lung disease, chronic bronchitis, emphysema, or asthma, subjects with febrile neutropenia, subjects with meningitis, subjects with septic arthritis, subjects with urinary tract infection, subjects with necrotizing fasciitis, subjects with other suspected Group A streptococcus infection, subjects who have had a splenectomy, subjects with recurrent or suspected enterococcus infection, other medical and surgical conditions associated with increased risk of infection, Gram positive sepsis, Gram negative sepsis, culture negative sepsis, fungal sepsis, meningococcemia, post-pump syndrome,

cardiac stun syndrome, myocardial infarction, stroke, congestive heart failure, hepatitis, epiglotittis, E. coli 0157:H7, malaria, gas gangrene, toxic shock syndrome, pre-eclampsia, eclampsia, HELP syndrome, mycobacterial tuberculosis, Pneumocystic carinii, pneumonia, Leishmaniasis, hemolytic uremic syndrome/thrombotic thrombocytopenic purpura, Dengue hemorrhagic fever, pelvic inflammatory disease, Legionella, Lyme disease, Influenza A, Epstein-Barr virus, encephalitis, inflammatory diseases and autoimmunity including Rheumatoid arthritis, osteoarthritis, progressive systemic sclerosis, systemic lupus erythematosus, inflammatory bowel disease, idiopathic pulmonary fibrosis, sarcoidosis, hypersensitivity pneumonitis, systemic vasculitis, Wegener's granulomatosis, transplants including heart, liver, lung kidney bone marrow, graft-versus-host disease, transplant rejection, sickle cell anemia, nephrotic syndrome, toxicity of agents such as OKT3, cytokine therapy, and cirrhosis.

49. The method or use of any one of claims 35-48, wherein the inflammatory condition is systemic inflammatory response syndrome.

50. The method or use of any one of claims 35-49, wherein the risk genotype is located at a polymorphic site at one or more of the following positions: 4732 of SEQ ID NO:1; 4054 of SEQ ID NO:2; or a polymorphic site in linkage disequilibrium thereto.

51. The method or use of any one of claims 35-50, wherein the risk genotype is located at a polymorphic site corresponding to position 2418 of SEQ ID NO:1 or a polymorphic site in linkage disequilibrium thereto.

52. The method or use of any one of claims 35-51, wherein the risk genotypes from the Protein C sequence and EPCR sequence are located at polymorphic sites at one or more of the following positions: 4732 of SEQ ID NO:1; 4054 of SEQ ID NO:2; 2418 of SEQ ID NO:1; or a polymorphic site in linkage disequilibrium thereto.

53. The method or use of claim 50 or 52, wherein the risk genotype is located at a polymorphic site in linkage disequilibrium with position 4732 is at position 4813, 6379, 6762, 7779, 8058, 8915 or 12228 of SEQ ID NO: 1.

54. The method or use of claim 50 or 52, wherein the risk genotype is located at a polymorphic site in linkage disequilibrium with position 4054 is at position 2973, 3063, 3402, 4946, 5515 or 6196 of SEQ ID NO: 2.

55. The method or use of claim 51 or 52, wherein the risk genotype is located at a

polymorphic site in linkage disequilibrium with position 2418 is at position 1386, 2583 or 3920 in SEQ ID NO: 1.

56. The method or use of claim 51 or 53, wherein the risk genotype located at a polymorphic site in linkage disequilibrium with position 4732 is a combination of two Protein C polymorphic sites, the combination being selected from the group of positions in SEQ ID NO: 1 consisting of:

9198 and 5867;
9198 and 4800;
3220 and 5867; and
3220 and 4800.

57. The method or use of claim 51 or 52, wherein the risk genotype located at a polymorphic site in linkage disequilibrium with position 2418 is a combination of two Protein C polymorphic sites, the combination being selected from the group of positions in SEQ ID NO: 1 consisting of:

5867 and 2405;
5867 and 4919;
5867 and 4956;
5867 and 6187;
5867 and 12109;
4800 and 2405;
4800 and 4919;
4800 and 4956;
4800 and 6187; and
4800 and 12109.

58. The method or use of any one of claims 50, 51, 52, 53, 55, 56 or 57, wherein the risk genotype is selected from the group of protein C single polymorphic sites and combined polymorphic sites in SEQ ID NO: 1 consisting of:

4732 C;
4813 A;
6379 G;
6762 A;
7779 C;
8058 T;
8915 T;
12228 T;
9198 C and 5867 A;
9198 C and 4800 G;
3220 A and 5867 A; and
3220 A and 4800 G

or

1386 T;
2418 A;
2583 A;
3920 T;
5867 A and 2405 T;
5867 A and 4919 A;
5867 A and 4956 T;
5867 A and 6187 C;
5867 A and 12109 T;
4800 G and 2405 T;
4800 G and 4919 A;
4800 G and 4956 T;
4800 G and 6187 C; and
4800 G and 12109 T.

59. The method or use of any one of claims 50, 52 or 54, wherein the genotype for an increased risk or risk genotype is selected from the group of EPCR polymorphic sites in SEQ ID NO: 2 consisting of:

6196 G;
5515 T;
4946 T;
4054 T;
3402 G;
3063 G; and
2973 C.

60. The method or use of any one of claims 58 or 59, wherein the genotype of the subject is indicative of an increased risk of poor outcome from an inflammatory condition.

61. The method or use of any one of claims 58, 59 or 60, wherein the subject having an increased risk of poor outcome from an inflammatory condition is preferentially selected for administration the anti-inflammatory agent or the anti-coagulant agent.

62. The method or use of any one of claims 50, 51, 52, 53, 55, 56 or 57, wherein the genotype for a decreased risk is selected from the group of protein C single polymorphic sites and combined polymorphic sites in SEQ ID NO: 1 consisting of:

4732 T;
4813 G;
6379 A;
6762 G;
7779 -;
8058 C;
8915 G;
12228 C;
9198 A and 5867 G;

9198 A and 4800 C;
3220 G and 5867 G; and
3220 G and 4800 C

or

1386 C;
2418 G;
2583 T;
3920 C;
5867 G and 2405 C;
5867 G and 4919 G;
5867 G and 4956 C;
5867 G and 6187 T;
5867 G and 12109 C;
4800 C and 2405 C;
4800 C and 4919 G;
4800 C and 4956 C;
4800 C and 6187 T; and
4800 C and 12109 C.

63. The method or use of any one of claims 50, 52 or 54, wherein the genotype for a decreased risk is selected from the group of EPCR polymorphic sites in SEQ ID NO: 2 consisting of:

6196 C;
5515 C;
4946 C;
4054 C;
3402 C;
3063 A; and
2973 T.

64. The method or use of any one of claims 62 or 63, wherein the genotype of the subject is indicative of a decreased risk of poor outcome from an inflammatory condition.

65. The method or use of any one of claims 62, 63 or 64, wherein the subject having a decreased risk of poor outcome from an inflammatory condition is preferentially not selected for administration the anti-inflammatory agent or the anti-coagulant agent.

66. The method or use of any one claims 35 to 65, wherein the anti-inflammatory agent or the anti-coagulant agent is selected from any one or more of the following:

(a) activated protein C;

(b) tissue factor pathway inhibitors;

(c) platelet activating factor hydrolase;

(d) PAF-AH enzyme analogues;

(e) antibody to tumor necrosis factor alpha;

(f) soluble tumor necrosis factor receptor-immunoglobulin G1;

(g) procysteine;

(h) elastase inhibitor;

(i) human recombinant interleukin 1 receptor antagonists; and

(j) antibodies, inhibitors and antagonists to endotoxin, tumour necrosis factor receptor, interleukin-6, high mobility group box, tissue plasminogen activator, bradykinin, CD-14 and interleukin-10.

67. The method or use of any one claims 35 to 66, wherein the anti-inflammatory agent or the anti-coagulant agent is activated protein C.

68. The method or use of any one claims 35 to 67, wherein the anti-inflammatory agent or the anti-coagulant agent is drotecogin alfa activated.

69. An oligonucleotide of about 10 to about 400 nucleotides that hybridizes specifically to a sequence contained in a human target sequence consisting of SEQ ID NO:1, a complementary sequence of the target sequence or RNA equivalent of the target sequence and wherein the oligonucleotide is operable in determining a polymorphism genotype at position 4732, 4813, 6379, 6762, 7779, 8058, 8915, 12228, 9198, 5867, 4800, 3220, 1386, 2418, 2583, 3920, 2405, 4919, 4956, 6187 or 12109 of SEQ ID NO:1.

70. An oligonucleotide of about 10 to about 400 nucleotides that hybridizes specifically to a sequence contained in a human target sequence consisting of SEQ ID NO:2, a complementary sequence of the target sequence or RNA equivalent of the target sequence and wherein the oligonucleotide is operable in determining a polymorphism genotype at position 6196, 5515, 4946, 4054, 3402, 3063 or 2973 of SEQ ID NO:2.

71. An oligonucleotide of about 10 to about 400 nucleotides that hybridizes specifically to a sequence contained in a human target sequence consisting of SEQ ID NO:1, a complementary sequence of the target sequence or RNA equivalent of the target sequence and wherein said hybridization is operable in determining a polymorphism genotype at position 4732, 4813, 6379, 6762, 7779, 8058, 8915,

12228, 9198, 5867, 4800, 3220, 1386, 2418, 2583, 3920, 2405, 4919, 4956, 6187 or 12109 of SEQ ID NO:1.

72. An oligonucleotide of about 10 to about 400 nucleotides that hybridizes specifically to a sequence contained in a human target sequence consisting of SEQ ID NO:2, a complementary sequence of the target sequence or RNA equivalent of the target sequence and wherein said hybridization is operable in determining a polymorphism genotype at position 6196, 5515, 4946, 4054, 3402, 3063 or 2973 of SEQ ID NO:2.

73. An oligonucleotide probe selected from the group consisting of:

(a) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 4732 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 4732;

(b) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 4732 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 4732;

(c) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 4813 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 4813;

(d) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 4813 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 4813;

(e) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 6379 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 6379;

(f) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 6379 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 6379;

(g) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 6762 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 6762;

(h) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 6762 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 6762;

(i) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 7779 but not to a nucleic acid molecule comprising SEQ ID NO:46 having a T at position 7779;
(j) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:46 having a T at position 7779 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 7779;
(k) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 8058 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 8058;
(l) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 8058 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 8058;
(m) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 8915 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 8915;
(n) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 8915 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 8915;
(o) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 12228 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 12228;
(p) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 12228 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 12228;
(q) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 5867 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 5867;
(r) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 5867 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 5867;
(s) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 9198 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 9198;

(t) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 9198 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 9198;

(u) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 4800 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 4800;

(v) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 4800 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 4800;

(w) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 3220 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 3220;

(x) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 3220 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 3220;

(y) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 2418 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 2418; and

(z) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 2418 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 2418.

74. An oligonucleotide probe selected from the group consisting of:

(a) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 2973 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 2973;

(b) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 2973 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 2973;

(c) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 3063 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a A at position 3063;

(d) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a A at position 3063 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 3063;

(e) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 3402 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 3402;

(f) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 3402 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 3402;

(g) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 4054 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 4054;

(h) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 4054 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 4054;

(i) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 4946 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 4946;

(j) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 4946 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 4946;

(k) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 5515 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 5515;

(l) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 5515 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 5515;

(m) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 6196 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 6196; and

(n) a probe that hybridizes under high stringency conditions to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 6196 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 6196.

75. An array of nucleic acid molecules attached to a solid support, the array comprising one or more oligonucleotides selected from the group consisting of:
(a) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 4732 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 4732;
(b) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 4732 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 4732;
(c) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 4813 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 4813;
(d) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 4813 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 4813;
(e) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 6379 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 6379;
(f) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 6379 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 6379;
(g) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 6762 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 6762;
(h) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 6762 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 6762;
(i) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 7779 but not to a nucleic acid molecule comprising SEQ ID NO:46 having a T at position 7779;
(j) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:46 having a T at position 7779 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 7779;

(k) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 8058 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 8058;

(l) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 8058 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 8058;

(m) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 8915 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 8915;

(n) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 8915 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 8915;

(o) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 12228 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 12228;

(p) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 12228 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a T at position 12228;

(q) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 5867 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 5867;

(r) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 5867 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 5867;

(s) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 9198 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 9198;

(t) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 9198 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 9198;

(u) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 4800 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 4800;

(v) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a C at position 4800 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 4800;

(w) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 3220 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 3220;

(x) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 3220 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 3220;

(y) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 2418 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 2418; and

(z) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:1 having a G at position 2418 but not to a nucleic acid molecule comprising SEQ ID NO:1 having a A at position 2418.

76. An array of nucleic acid molecules attached to a solid support, the array comprising one or more oligonucleotides selected from the group consisting of:

(a) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 2973 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 2973;

(b) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 2973 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 2973;

(c) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 3063 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a A at position 3063;

(d) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a A at position 3063 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 3063;

(e) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 3402 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 3402;

(f) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 3402 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 3402;

(g) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 4054 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 4054;

(h) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 4054 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 4054;

(i) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 4946 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 4946;

(j) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 4946 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 4946;

(k) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 5515 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 5515;

(l) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 5515 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a T at position 5515;

(m) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 6196 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 6196; and

(n) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:2 having a C at position 6196 but not to a nucleic acid molecule comprising SEQ ID NO:2 having a G at position 6196.

77. An array of nucleic acid molecules attached to a solid support, the array comprising one or more oligonucleotides selected from the group consisting of:

(a) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:3 having a G at position 201 but not to a nucleic acid molecule represented by the same SEQ ID NO having a A at position 201;

(b) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:3 having a A at position 201 but not to a nucleic acid molecule represented by the same SEQ ID NO having a G at position 201;

(c) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:4, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:18, SEQ ID NO:19, or SEQ ID NO:20 having a T at position 201 but not to a nucleic acid molecule represented by the same SEQ ID NO having a C at position 201;

(d) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:4, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:18, SEQ ID NO:19, or SEQ ID NO:20 having a C at position 201 but not to a nucleic acid molecule represented by the same SEQ ID NO having a T at position 201;

(e) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:5, SEQ ID NO:17, or SEQ ID NO:21 having a C at position 201 but not to a nucleic acid molecule represented by the same SEQ ID NO having a G at position 201;

(f) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:5, SEQ ID NO:17, or SEQ ID NO:21 having a G at position 201 but not to a nucleic acid molecule represented by the same SEQ ID NO having a C at position 201;

(g) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:12 having a G at position 201 but not to a nucleic acid molecule comprising SEQ ID NO:12 having a T at position 201;

(h) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:12 having a T at position 201 but not to a nucleic acid molecule comprising SEQ ID NO:12 having a G at position 201;

(i) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:12 having a T at position 201 but not to a nucleic acid molecule comprising SEQ ID NO:12 having a G at position 201; and

(j) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:13 having a A at position 201 but not to a nucleic acid molecule comprising SEQ ID NO:13 having a C at position 201.

78. An array of nucleic acid molecules attached to a solid support, the array comprising one or more oligonucleotides selected from the group consisting of:

(a) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:22, SEQ ID NO:23, or SEQ ID NO:41 having a C at position 15 but not to a nucleic acid molecule represented by the same SEQ ID NO having a G at position 15;

(b) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:22, SEQ ID NO:23, or SEQ ID NO:41 having a G at position 15 but not to a nucleic acid molecule represented by the same SEQ ID NO having a C at position 15;

(c) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:24, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:39, or SEQ ID NO:44 having a C at position 15 but not to a nucleic acid molecule represented by the same SEQ ID NO having a G at position 15;

(d) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:24, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:39, or SEQ ID NO:44 having a G at position 15 but not to a nucleic acid molecule represented by the same SEQ ID NO having a C at position 15;

(e) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:25 or SEQ ID NO:49 having a A at position 15 but not to a nucleic acid molecule represented by the same SEQ ID NO having a T at position 15;

(f) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:25 or SEQ ID NO:49 having a T at position 15 but not to a nucleic acid molecule represented by the same SEQ ID NO having a A at position 15;

(g) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:26, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:38, or SEQ ID NO:40 having a A at position 15 but not to a nucleic acid molecule represented by the same SEQ ID NO having a G at position 15;

(h) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:26, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:38, or SEQ ID

NO:40 having a G at position 15 but not to a nucleic acid molecule represented by the same SEQ ID NO having a A at position 15;

(i) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:37, SEQ ID NO:42, or SEQ ID NO:43 having a C at position 15 but not to a nucleic acid molecule represented by the same SEQ ID NO having a A at position 15; and

(j) an oligonucleotide that will hybridize to a nucleic acid molecule comprising SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:37, SEQ ID NO:42, or SEQ ID NO:43 having a A at position 15 but not to a nucleic acid molecule represented by the same SEQ ID NO having a C at position 15.

79. An array of nucleic acid molecules attached to a solid support, the array comprising an oligonucleotide that will hybridize to a nucleic acid molecule consisting of SEQ ID NO:1, wherein the nucleotide at position 4732 is C, under conditions in which the oligonucleotide will not substantially hybridize to a nucleic acid molecule consisting of SEQ ID NO:1 wherein the nucleotide at position 4732 is T.

80. An array of nucleic acid molecules attached to a solid support, the array comprising an oligonucleotide that will hybridize to a nucleic acid molecule consisting of SEQ ID NO:1, wherein the nucleotide at position 4732 is T, under conditions in which the oligonucleotide will not substantially hybridize to a nucleic acid molecule consisting of SEQ ID NO:1 wherein the nucleotide at position 4732 is C.

81. An array of nucleic acid molecules attached to a solid support, the array comprising an oligonucleotide that will hybridize to a nucleic acid molecule consisting of SEQ ID NO:2, wherein the nucleotide at position 4054 is T, under conditions in which the oligonucleotide will not substantially hybridize to a nucleic acid molecule consisting of SEQ ID NO:2 wherein the nucleotide at position 4054 is C.

82. An array of nucleic acid molecules attached to a solid support, the array comprising an oligonucleotide that will hybridize to a nucleic acid molecule consisting of SEQ ID NO:1, wherein the nucleotide at position 4054 is C, under conditions in which the oligonucleotide will not substantially hybridize to a nucleic acid molecule consisting of SEQ ID NO:1 wherein the nucleotide at position 4054

is T.

83. The oligonucleotide of any one of claims 69 to 82, further comprising one or more of the following: a detectable label; a quencher; a mobility modifier; a contiguous non-target sequence situated 5' or 3' to the target sequence or 5' and 3' to the target sequence.

84. A computer readable medium comprising a plurality of digitally encoded genotype correlations selected from the Protein C and EPCR genotype correlations in TABLE 1E, wherein each correlation of the plurality has a value representing an ability to recover from an inflammatory condition and an indication of responsiveness to treatment of an inflammatory condition with an anti-inflammatory agent or an anti-coagulant agent.